

Resource Summary Report

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euHCVdb: The European HCV database

RRID:SCR_007645

Type: Tool

Proper Citation

euHCVdb: The European HCV database (RRID:SCR_007645)

Resource Information

URL: <http://euhcvdb.ibcp.fr>

Proper Citation: euHCVdb: The European HCV database (RRID:SCR_007645)

Description: THIS RESOURCE IS NO LONGER IN SERVICE, documented May 10, 2017. A pilot effort that has developed a centralized, web-based biospecimen locator that presents biospecimens collected and stored at participating Arizona hospitals and biospecimen banks, which are available for acquisition and use by researchers. Researchers may use this site to browse, search and request biospecimens to use in qualified studies. The development of the ABL was guided by the Arizona Biospecimen Consortium (ABC), a consortium of hospitals and medical centers in the Phoenix area, and is now being piloted by this Consortium under the direction of ABRC. You may browse by type (cells, fluid, molecular, tissue) or disease. Common data elements decided by the ABC Standards Committee, based on data elements on the National Cancer Institute's (NCI's) Common Biorepository Model (CBM), are displayed. These describe the minimum set of data elements that the NCI determined were most important for a researcher to see about a biospecimen. The ABL currently does not display information on whether or not clinical data is available to accompany the biospecimens. However, a requester has the ability to solicit clinical data in the request. Once a request is approved, the biospecimen provider will contact the requester to discuss the request (and the requester's questions) before finalizing the invoice and shipment. The ABL is available to the public to browse. In order to request biospecimens from the ABL, the researcher will be required to submit the requested required information. Upon submission of the information, shipment of the requested biospecimen(s) will be dependent on the scientific and institutional review approval. Account required. Registration is open to everyone., documented August 23, 2016. The euHCVdb is oriented towards protein sequence, structure, function analysis and structural biology of the Hepatitis C Virus. It is monthly updated from the EMBL Nucleotide sequence database and maintained in a relational database management system (PostgreSQL). Programs for parsing the EMBL database flat files, annotating HCV entries, filling up and querying the database used SQL and Java programming languages. Great efforts have been made to develop a fully automatic annotation procedure thanks to a reference set of HCV complete annotated well-characterized genomes of various

genotypes. This automatic procedure ensures standardization of nomenclature for all entries and provides genomic regions/proteins present in the entry, bibliographic reference, genotype, interesting sites (e.g. HVR1) or domains (e.g. NS3 helicase), source of the sequence (e.g. isolate) and structural data that are available as protein 3D models. The euHCVdb is funded as part of the HepCVax cluster (EC grant QLK2-CT-2002-01329) and viRgil network of excellence (EC grant LSHM-CT-2004-503359).

Synonyms: euHCVdb

Resource Type: data or information resource, database

Keywords: hcv, hepatitis c virus

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: euHCVdb: The European HCV database

Resource ID: SCR_007645

Alternate IDs: nif-0000-02819, r3d100011795

Alternate URLs: <https://doi.org/10.17616/R3R044>, <https://doi.org/10.17616/R3R044>

Record Creation Time: 20220129T080243+0000

Record Last Update: 20260821T193815+0000

Ratings and Alerts

No rating or validation information has been found for euHCVdb: The European HCV database.

No alerts have been found for euHCVdb: The European HCV database.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 7 mentions in open access literature.

Listed below are recent publications. The full list is available at [dkNET](#) .

Kliemann DA, et al. (2016) Polymorphisms and resistance mutations of hepatitis C virus on sequences in the European hepatitis C virus database. World journal of gastroenterology, 22(40), 8910.

Kliemann DA, et al. (2016) Genetic Barrier to Direct Acting Antivirals in HCV Sequences Deposited in the European Databank. PloS one, 11(8), e0159924.

Gouttenoire J, et al. (2014) Aminoterminal amphipathic α -helix AH1 of hepatitis C virus nonstructural protein 4B possesses a dual role in RNA replication and virus production. PLoS pathogens, 10(10), e1004501.

Jirasko V, et al. (2010) Structural and functional studies of nonstructural protein 2 of the hepatitis C virus reveal its key role as organizer of virion assembly. PLoS pathogens, 6(12), e1001233.

Hanouille X, et al. (2009) Domain 3 of non-structural protein 5A from hepatitis C virus is natively unfolded. Biochemical and biophysical research communications, 381(4), 634.

Wolf M, et al. (2008) The major form of hepatitis C virus alternate reading frame protein is suppressed by core protein expression. Nucleic acids research, 36(9), 3054.

de Chassey B, et al. (2008) Hepatitis C virus infection protein network. Molecular systems biology, 4, 230.